MULTIBREED BREEDING VALUE ESTIMATION BASED ON WEANING RESULTS IN A BEEF HERD IN HUNGARY

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SUMMARY

Weaning results of 886 calves (438 males and 448 females; 613 purebred and 273 crossbred) born from 10 dam breeds (Hungarian Simmental, Hungarian Grey, Hereford, Aberdeen and Red Angus, Lincoln Red, Shaver, Limousin, Charolais, Blonde d'Aquitaine), kept between 1997-2012 under the same condition on peat-bog soil pasture at Keszthely were evaluated. Population genetics parameters, variance, covariance components, heritability values, correlation coefficients and breeding values were estimated in several different genotypes containing (multibreed) population. Three different sire models and three different animal models were used for the estimation. The direct heritability (h^2_d) of birth weight, weaning weight, preweaning daily gain and 205-day weight was between 0.18 and 0.39, the maternal heritability (h^2_m) of these traits was 0.00 and 0.16. The direct-maternal correlations (r_{dm}) in weaning weight, preweaning daily gain and 205-day weight were -0.36 and -0.63. The total heritability values were between 0.18 and 0.29. The results obtained with six different BLUP models were similar to each other with a little difference. These results demonstrate that, with the sire model and with the animal model estimated rankings are very similar to each other. The rank-correlation between the sire and animal models was medium or strong and positive (r_{rank} = 0.62 - 0.80; $p<0.01$). The models affected the breeding value of animals insignificantly. Among the rankings no differences were found between sire and animal model. It can be concluded that under the same condition simple models give reliable results.

ÖSSZEFOGLALÁS

Bene Sz. - Giczi A. - Rádli A. - Polgár J. P. - Szabó F.: TÖBBFAJTÁS TENYÉSZÉRTÉKBECSLÉS A VÁLASZTÁSI EREDMÉNYEK ALAPJÁN EGY HAZAI HÚSMARHA ÁLLOMÁNYBAN

A Szerzők a keszthelyi extenzív lápterületi legelőn, azonos körülmények között tartott 10 húsmarha fajta (magyar tarka, magyar szürke, hereford, aberdeen angus, red angus, lincoln red, shaver, limousin, charolais, blonde d'aquitaine) 1997 és 2012 között született 886 borjának (438 bika és 448 üsző; 613 fajtatiszta és 273 F_1-es) a választási eredményét értékelték. A munka során variancia és kovariancia komponenseket, örökölhetőségi értékeket, korrelációs együtthatókat, valamint tenyészértékeket számítottak a különböző genotípusú populációban. Az értékelést három-három különböző apa-, ill. egyedmodellel végezték. A születési súly, a választási súly, a választás előtti napi súlygyarapodás és a 205-napos súly direkt örökölhetősége (h^2_d) 0,18 - 0,39 közötti közepes, anyai örökölhetősége (h^2_m) 0,00 - 0,16 gyenge volt. A direkt és az anyai genetikai hatás közötti korrelációt (r_{dm}) a választási súly, a választás előtti napi súlygyarapodás, valamint a 205-napos súly esetén negatívnak, -0,36 és -0,63 közöttinek találták. A teljes örökölhetőség (h^2_T) 0,18 - 0,29 közötti volt. A hat különböző BLUP modell nagyon kis eltérésekkel hasonló eredményeket mutatott. A rang-korreláció vizsgálat az apa- és egyedmodellek között közepes, ill. szoros pozitív értékeket eredményezett (r_{rang} = 0,62 - 0,80; $p<0,01$). A vizsgálat során használt különböző modellek csak nagyon kis mértékben befolyásolták a tenyészértékeket. Az apa- és az egyedmodellel becsült rangsorok között nem találtak számottevő különbséget. Az eredmények alapján arra lehet következtetni, hogy azonos körülmények között tartott állományban az egyszerűbb modellekkel is megbízható eredményeket kaphatunk.

INTRODUCTION AND LITERATURE REVIEW

There are great interests for multibreed breeding value estimation among beef cattle breeders because most of them have commercial herds. Multibreed breeding value estimation means that it occurs for different breeds or crossbred populations in the same time from the same database. By using of multibreed breeding value estimation the estimated breeding value is much more exact because this method takes not only the additive genetic effects but nonadditive effects such as dominance, super dominance and ephystasis into consideration. Moreover, this method considers breed differences and the heterosis effects, too. The advantage of the multibreed breeding value estimation is that it gives different breeding values for a sire whether it is used for purebreeding or crossbreeding purpose.

Notter and Cundiff (1991) were among the first who published results of multibreed breeding value estimation. *Rodríguez-Almeida et al.* (1997) drew attention to increasing importance of multibreed breeding value estimation. During the years more and more new methods were developed for more appropriate estimation (*Elzo and Famula*, 1985; *Arnold et al.*, 1992; *Van Vleck et al.*, 1992; *Meyer et al.*, 1993; *Pollak and Quaas*, 1998; *Tőzsér et al.*, 2003; *Nagy et al.*, 2008; *Radnóczi et al.*, 2009 etc.).

Population genetic parameters of weaning traits of mixed populations were published by several authors (*Ahunu et al.*, 1997; *Crews and Kemp*, 1999; *Duangjinda et al.*, 2001; *Gutiérrez et al.*, 2007). The heritability values in these publications were 0.2 - 0.4.

According to some authors there are differences in genetic parameters between purebred and crossbred populations (*Splan et al.*, 1998, 2002; *Sullivan et al.*, 1999; *Newman et al.*, 2002). Generally values of direct-maternal genetic correlation (r_{dm}) in crossbred populations are lower than in purebred populations. However, *Gregory et al.* (1995) and *Szabó* (1993) found that there are no differences in genetic variance and hereditability values between purebred and crossbred populations when they are kept in the same conditions.

The purpose of the present study was to do breeding value estimation for multibreed population consists of ten breeds kept in the same herd for 16 years in our experimental farm. Since it is very rare to have so many breeds in the same environment such a long period, our result may have command interest.

MATERIALS AND METHODS

Research was carried out for period 1997-2012. The evaluated population was kept in peatbog soil pasture in the experimental farm of Georgikon Faculty of University of Pannon. There were ten breeds (Hungarian Simmental, Hungarian Grey, Hereford, Aberdeen Angus, Red Angus, Lincoln Red, Shaver, Limousin, Charolais, Blonde d'Aquitaine) as purebred and crossbred herds kept there in the same herd, same condition involved in the estimation.

Mating of cows and breeding heifers were organised seasonally. Artificial insemination was used to obtain purebred progeny while natural service for crossbred offspring. Calves were kept in the herds together with cows. Birth weight (on the

day of calving) and weaning weight (approximately 6-7 month of age) was taken individually.

The evaluated population consisted of 33 sires and 264 cows. They had 886 offspring's (438 males and 448 females; 613 purebred and 273 crossbred) calves between 1997 and 2012. The distribution of calves by years breeds and genotypes are summarised in *Table 1* and *Table 2*, while their pedigree in *Table 3*. In the farm breeding bulls are not rearing, so paternal grand dams and sires were not in the database.

Table 1

Number of calves according to breed of dam and birth year

Birth year (1)	Breed of dam (2)										Total (3)
	HS	HG	HE	AA	RA	LR	SH	LI	CH	BD	
1997	10		23	10	12	7					62
1998	6		35	8	8	1	2				60
1999	19		34	7	10	8	6				84
2000	10		14	6	7	6	3				46
2001	6		13	9	10	3	3			5	49
2002	14		18	9	15	3	6	5		4	74
2003	8		18	7	12	2	4	4	12	4	71
2004	14		11	8	10	2	4	1	10	1	61
2005	10		8	7	11		1	3	6	1	47
2006	12		9	5	7	1	2	1	10	2	49
2007	12		10	6	15	1	1	3	7	3	58
2008	8	10	6	3	12	3		2	1		45
2009	6	10	3	1	6	1	2	2	7		38
2010	9	8	2	5	8				2		34
2011	14	9	5	4	11		1	3	4	2	53
2012	13	9	6	5	14			2	6		55
Total	171	46	215	100	168	38	35	26	65	22	886

HS = Hungarian Simmental (4); HG = Hungarian Grey (5); HE = Hereford; AA = Aberdeen Angus; RA = Red Angus; LR = Lincoln Red; SH = Shaver; LI = Limousin; CH = Charolais; BD = Blonde d'Aquitaine

1. táblázat A borjak száma az anya fajtája és a születési év szerint
születési év (1); anya fajtája (2); összesen (3); magyar tarka (4); magyar szürke (5)

There were four traits, birth weight (BW), weaning weight (WW), preweaning daily gain (PDG) and 205-day weight (CWW) evaluated. Weaning age (WA), preweaning daily gain (PDG) and 205-day weaning weight (CWW) were calculated as follows:

$$WA\ (day) = Date\ of\ weaning - Date\ of\ birth$$
$$PDG\ (kg/day) = (WW - BW) / WA$$
$$CWW\ (kg) = (WW - BW) / WA \times 205 + BW$$

Table 2

Distribution of calves according to breed of sire and breed of dam

Breed of dam (1)	Breed of sire (2)									Total (3)
	HS	HG	HE	AA	RA	LR	LI	CH	BD	
HS	103		39		6		11		12	171
HG		46								46
HE	8		202	5						215
AA			27	51					22	100
RA	7		22		123		16			168
LR	10				25	3				38
SH	8				27					35
LI							19		7	26
CH	8							50	7	65
BD							6		16	22
Total	144	46	290	56	181	3	52	50	64	886

HS = Hungarian Simmental (4); HG = Hungarian Grey (5); HE = Hereford; AA = Aberdeen Angus; RA = Red Angus; LR = Lincoln Red; SH = Shaver; LI = Limousin; CH = Charolais; BD = Blonde d'Aquitaine

2. táblázat A borjak eloszlása az apa és az anya fajtája szerint
anya fajtája (1); apa fajtája (2); összesen (3); magyar tarka (4); magyar szürke (5)

Table 3

The composition of the examined population

Designation (1)	Number of animals (13)
Number of animals in total (2)	1094
Number of animals with records (3)	886
Sires (4)	33
Dams (5)	264
Paternal grand sire (6)	0
Maternal grand sires (7)	27
Total grand sires (8)	27
Paternal grand dams (9)	0
Maternal grand dams (10)	72
Total grand dams (11)	72
Calf without own performance	0

3. táblázat A vizsgált populáció összetétele
megnevezés (1); összes egyed (2); összes borjú (3); apa (4); anya (5); apai nagyapa (6); anyai nagyapa (7); összes nagyapa (8); apai nagyanya (9); anyai nagyanya (10); összes nagyanya (11); borjú saját teljesítmény nélkül (12); egyedszám (13)

Method of multibreed breeding value estimation in this study was similar to method used by *Van Vleck et al.* (1992), *Núnez-Dominguez et al.* (1993, 1995), *Splan et al.* (2002), and *Roso et al.* (2005). Population genetic parameters, variance, covariance components were estimated using BLUP. Three sire models

and three animal models, altogether six models were set up for the estimation. The differences between different models, similarly to models used by *Splan et al.* (2002) were the fixed effects (*Table 4*). Animal models contained the maternal genetic effects (*Cameron*, 1997) and the permanent maternal environmental effects (*Falconer and Trudy*, 1996). Weaning age as a covariant was taken - by weaning weight and preweaning daily gain - into consideration.

The sire model presented according to model 1 of weaning weight (*Szőke and Komlósi*, 2000) (where: $Y_{ijklmno}$ = weaning weight of calf from „i" sire, „j" genotype, in „k" year, in „l" season, from „m" year age dam, „n" sex, „o" day age; μ = overall mean value; S_i = random effect of sire; G_j = fix effect of genotype; Y_k = fix effect of year; E_l = fix effect of season; C_m = fix effect of age of dam at calving; I_n = fix effect of sex of calf; b = regression coefficient; $e_{ijklmno}$ = residual):

$$Y_{ijklmno} = \mu + S_i + G_j + Y_k + E_l + C_m + I_n + b(x_{ijklmno}\text{-}X) + e_{ijklmno}$$

With sire model estimated the additive direct genetic variance (σ^2_d), error (environmental) variance (σ^2_e), phenotypic variance (σ^2_p) and direct heritability (h^2_d).

Table 4

The statistical models

Effects (1)	Used BLUP (sire and animal) models (2)		
	Model 1	Model 2	Model 3
Breed of sire (3)	-	-	+
Breed of dam (4)	-	+	+
Genotype of calf (5)	+	+	-
Age of dam at calving (6)	+	+	+
Birth year of calf (7)	+	+	+
Birth season of calf (8)	+	+	+
Sex of calf (9)	+	+	+

+ = part of the model (10); - = the model doesn't include this effect (11)

4. táblázat Az alkalmazott modellek
hatások (1); az alkalmazott BLUP (apa és egyed) modellek (2); apa fajtája (3); anya fajtája (4); borjú genotípusa (5); anya elléskori életkora (6); borjú születési éve (7); borjú születési évszaka (8); borjú ivara (9); a modell ezt a hatást tartalmazza (10); a modell ezt a hatást nem tartalmazza (11)

The general form of the animal models can be written as follows (where: y = the observation vector (trait); b = vector of fix effect(s); u = vector of random effect (animal); m = vector of maternal genetic effect; pe = vector of maternal permanent environmental effect; e = error vector; X = incidence matrix of fixed effects; Z = incidence matrix of random effects; W = incidence matrix of maternal genetic effect; S = incidence matrix of maternal permanent environmental effect):

$$y = Xb + Zu + Wm + Spe + e$$

Estimation with animal model the following population genetic parameters, covariance and variance components were determined: additive direct genetic variance (σ^2_d), maternal genetic variance (σ^2_m), direct-maternal genetic covariance (σ_{dm}), maternal permanent environmental effect (σ^2_{pe}), residual variance (σ^2_e), phenotypic variance (σ^2_p), direct heritability (h^2_d), maternal heritability (h^2_m), direct-maternal genetic correlation (r_{dm}), the ratio of the permanent environmental variance to the phenotypic variance (c^2) and the ratio of the residual variance to the phenotypic variance (e^2). The total heritability (h^2_T) was calculated using the following formula (*Willham*, 1972):

$$h^2_T = (\sigma^2_d + 0{,}5\ \sigma^2_m + 1{,}5\ \sigma_{dm}) / \sigma^2_p$$

Three animal models were compared on the basis of „-2 log likelihood" values. Those model was considered to be the most accurate in which the „-2 log likelihood" value was the lowest (*Splan et al.*, 2002; *Roso et al.*, 2005).

Breeding value was estimated for 33 sires. Based on breeding values sires were ranked using three type of rank-correlation according to *Núnez-Dominguez et al.* (1995) and *Lengyel* (2005).

The genetic trend of weaning results was stated according to the means of breeding values referring to the year of birth (*Bene et al.*, 2007, 2010). The animal model estimates a breeding value for each animal (dam, sire, calf). To determine the genetic trend the breeding value of the animal, born in the same year based on the direct genetic effect was averaged and the obtained points were represented in a system of co-ordinates.

Microsoft Excel 2003 and Microsoft Word 2003 were used for arranging data, while Harvey (1990) sire model and DFREML (*Meyer*, 1998) and MTDFREML (*Boldman et al.*, 1993) animal models were used for the estimation.

RESULTS AND DISCUSSION

The mean values of the evaluated traits are summarized in *Table 5*. In purebred population highest birth weight (41.3 kg), weaning weight (225.4 kg), daily gain (0.896 kg/day) and 205-day weaning weight (225.0 kg) were reached by Blonde d'Aquitaine calves. The lowest values were obtained by purebred Hereford calves (29.6 kg, 156.4 kg, 0.629 kg/day and 157.9 kg, respectively). In case of crossbred population highest 205-day weaning weight (CWW) was reached by Red Angus x Hungarian Simmental F_1 calves, while the lowest by Lincoln Red x Hungarian Simmental F_1 calves (160.0 kg).

Table 6 and *Table 7* contain the population genetic parameters, variance and covariance components estimated by six different BLUP models. Direct heritability (h^2_d) values were between 0.18 and 0.39. These results are similar to that Lengyel (2005) found in purebred population. There were a little bit lower heredity (h^2) values in crossbred populations obtained by *Van Vleck et al.* (1996), *Crews and Kemp* (1999) and *Splan et al.* (1998, 2002). However, no differences were found in results between sire model and animal model. Animal model gave lower error than sire model.

Table 5

The weaning results of different genotype calves

Genotype of calves (1)	N	Birth weight (kg) (2)		Weaning weight (kg) (3)		Preweaning daily gain (kg/day) (4)		205-day weight (kg) (5)	
		Mean (6)	s	Mean	s	Mean	s	Mean	s
Purebred (7)									
HS	103	34.9	4.79	213.4	65.93	0.832	0.26	205.3	53.43
HG	46	31.6	2.68	151.7	50.59	0.657	0.14	166.7	29.04
HE	202	29.6	5.29	156.4	49.20	0.629	0.25	157.9	52.29
AA	51	32.4	5.55	204.6	72.68	0.874	0.25	211.2	50.46
RA	123	33.2	4.53	214.3	58.11	0.883	0.23	214.7	49.02
LR	3	31.3	4.16	180.0	40.51	0.863	0.03	208.2	8.01
LI	19	33.4	4.55	186.7	54.19	0.854	0.21	209.2	41.21
CH	50	38.4	5.51	188.3	52.02	0.805	0.17	203.5	33.84
BD	16	41.3	5.22	225.4	71.84	0.896	0.23	225.0	49.53
Crossbred (8)									
HS x HE	39	34.3	4.28	163.2	35.51	0.678	0.22	173.3	43.59
HS x RA	6	35.8	3.54	202.5	32.07	0.871	0.16	214.7	32.27
HS x LI	11	35.9	2.59	200.6	44.18	0.735	0.15	188.1	28.62
HS x BD	12	37.0	5.22	256.5	36.65	1.032	0.24	248.6	48.94
HE x HS	8	30.0	2.56	204.3	71.09	0.880	0.24	210.4	51.30
HE x AA	5	31.0	2.12	171.0	39.37	0.717	0.16	179.5	32.76
AA x HE	27	31.1	3.36	170.0	44.62	0.795	0.19	194.0	41.75
AA x BD	22	37.5	5.16	195.3	42.36	0.970	0.17	236.5	34.35
RA x HS	7	34.0	3.74	218.0	85.03	1.179	0.25	275.7	53.86
RA x HE	22	31.7	3.82	184.5	38.13	0.841	0.25	204.1	50.93
RA x LI	16	33.6	4.75	178.4	42.62	0.939	0.26	226.1	55.44
LR x HS	10	34.6	2.80	168.5	45.21	0.612	0.11	160.0	23.85
LR x RA	25	33.7	4.58	144.4	39.01	0.676	0.26	172.6	55.50
SH x HS	8	34.8	5.60	243.9	40.77	0.831	0.16	205.0	35.17
SH x RA	27	36.6	5.34	198.3	42.56	0.868	0.21	214.7	44.37
LI x BD	7	39.1	4.81	218.4	72.82	1.061	0.22	256.6	42.57
CH x HS	8	37.0	3.70	222.4	74.19	0.963	0.12	235.7	23.69
CH x BD	7	38.1	6.04	253.9	64.84	1.088	0.29	261.6	60.63
BD x LI	6	38.0	5.55	177.3	69.67	0.792	0.38	201.1	71.89
Total (9)	886	33.3	5.52	187.2	60.34	0.787	0.26	194.7	54.44

HS = Hungarian Simmental (10); HG = Hungarian Grey (11); HE = Hereford; AA = Aberdeen Angus; RA = Red Angus; LR = Lincoln Red; SH = Shaver; LI = Limousin; CH = Charolais; BD = Blonde d'Aquitaine

5. táblázat A különböző genotípusú borjak választási eredményei

borjú genotípusa (1); születési súly (2); választási súly (3); választás előtti napi súlygyarapodás (4); 205-napos súly (5); átlag (6); fajtatiszta (7); keresztezett (8); összesen (9); magyar tarka (10); magyar szürke (11)

The maternal heritability (h^2_m) values varied between 0.00 and 0.16. These results are similar to the results of *Núnez-Dominguez et al.* (1993), *Van Vleck et al.* (1996), *Dodenhoff et al.* (1999) and *Gutiérrez et al.* (2007). Covariance between direct additive genetic effects and maternal genetic effects were negative with exception of birth weight. The correlation coefficients (r_{dm}) were loose and negative values between -0.36 and -0.63. These results are similar to findings of *Splan et al.* (2002) and *Ahunu et al.* (1997) in crossbred populations, moreover to results of *Dodenhoff et al.* (1999), obtained in purebred population. At the same time *Cubas et al.* (1991), *Roso et al.* (2005) found closer correlation values between direct additive genetic effects.

Total heritability values (h^2_T) of the studied traits were between 0.18 - 0.29. This result is similar to that which was found in crossbred population by *Meyer* (1998), furthermore *Bennett and Gregory* (2001).

Based on the comparison of the accuracy - compared according to *Splan et al.* (2002) and *Roso et al.* (2005) -, of the three animal models only a small difference were found between them. Since, the lowest „-2 log likelihood" value were found for model 2, this model was used for the further estimation.

Table 8 shows the breeding values of the studied sires according to additive direct genetic effect obtained by both sire model and animal model. As seen there are meaningful differences between results received by different models, namely sire model resulted higher breeding value data than animal model. However, their indication, negative or positive was the same in case of two models.

Table 9 contains the rank of 33 sires based on their breeding value. In spite of big differences between results by different models the rank of sires was similar in case of both models. The best breeding value for weaning weight (+52.51 kg) by sire model was obtained by a "14765" registration number Limousin sire. However, by animal model he had +13.26 kg breeding value, which value resulted the second place in the rank.

The models were compared with rank correlation analysis (*Table 10*). The obtained rank correlation coefficients demonstrate that the different model estimated rankings are very similar in weaning weight, similar in birth weight, preweaning daily gain and 205-day weight. It appears that under same conditions the model is not or only very slightly affected the rank of animals.

Table 6

Estimated genetic parameters, variance and covariance components I

Trait (1)	Genetics parameters (2)	Sire model (3)			Animal model (4)		
		Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
BW	σ^2_d	9.0	7.8	7.8	5.2	5.1	4.7
	σ^2_m	-	-	-	0.0	0.0	0.0
	σ_{dm}	-	-	-	0.0	0.0	0.0
	σ^2_{pe}	-	-	-	0.01	0.01	0.01
	σ^2_e	15.7	15.7	15.8	12.5	12.5	12.8
	σ^2_p	24.7	23.5	23.6	17.7	17.6	17.6
	h^2_d	0.36±0.19	0.33±0.19	0.33±0.19	0.29±0.13	0.29±0.13	0.27±0.13
	h^2_m	-	-	-	0.00±0.07	0.00±0.07	0.00±0.07
	r_{dm}	-	-	-	0.00±0.00	0.00±0.00	0.00±0.00
	c^2	-	-	-	0.00±0.07	0.00±0.06	0.00±0.06
	e^2	-	-	-	0.71±0.10	0.71±0.11	0.73±0.10
	$h^2_m+c^2$	-	-	-	0.00	0.00	0.00
	h^2_T	-	-	-	0.29	0.29	0.27
	-2 log l	-	-	-	3334	3313	3355
WW	σ^2_d	447	446	499	383	376	481
	σ^2_m	-	-	-	210	200	217
	σ_{dm}	-	-	-	-148	-136	-173
	σ^2_{pe}	-	-	-	0.06	0.08	0.07
	σ^2_e	1199	1197	1201	876	874	822
	σ^2_p	1646	1643	1700	1321	1317	1347
	h^2_d	0.27±0.19	0.27±0.19	0.29±0.20	0.29±0.17	0.29±0.17	0.36±0.20
	h^2_m	-	-	-	0.16±0.14	0.15±0.14	0.16±0.15
	r_{dm}	-	-	-	-0.52±0.35	-0.49±0.36	-0.53±0.31
	c^2	-	-	-	0.00±0.07	0.00±0.07	0.00±0.07
	e^2	-	-	-	0.66±0.13	0.66±0.13	0.61±0.15
	$h^2_m+c^2$	-	-	-	0.16	0.15	0.16
	h^2_T	-	-	-	0.20	0.21	0.24
	-2 log l	-	-	-	6889	6849	6955

BW = birth weight (5); WW = weaning weight (6)

σ^2_d = additive direct genetic variance (7); σ^2_m = maternal genetic variance (8); σ_{dm} direct maternal genetic covariance (9); σ^2_{pe} = maternal permanent environmental effect (10); σ^2_e = residual variance (11); σ^2_p = phenotypic variance (12); h^2_d = direct heritability (13); h^2_m = maternal heritability (14); r_{dm} = direct-maternal genetic correlation (15); c^2 = the ratio of the permanent environmental variance to the phenotypic variance (16); e^2 = the ratio of the residual variance to the phenotypic variance (17); h^2_T = total heritability (18)

6. táblázat A becsült genetikai paraméterek, variancia és kovariancia komponensek I.
tulajdonság (1); genetikai paraméter (2); apamodell (3); egyedmodell (4); születési súly (5); választási súly (6); direkt additív genetikai variancia (7); anyai genetikai variancia (8); direkt-anyai kovariancia (9); anyai állandó környezeti variancia (10); hiba variancia (11); fenotípusos variancia (12); direkt örökölhetőség (13); anyai örökölhetőség (14); direkt-anyai genetikai korreláció (15); állandó környezeti variancia aránya a fenotípusban (16); hiba variancia aránya a fenotípusban (17); teljes örökölhetőség (18)

Table 7

Estimated genetic parameters, variance and covariance components II

Trait (1)	Genetics parameters (2)	Sire model (3)			Animal model (4)		
		Model 1	Model 2	Model 3	Model 1	Model 2	Model 3
PDG	σ^2_d	0.0071	0.0072	0.0089	0.0078	0.0080	0.0106
	σ^2_m	-	-	-	0.0020	0.0023	0.0021
	σ_{dm}	-	-	-	-0.0014	-0.0019	-0.0022
	σ^2_{pe}	-	-	-	0.0000	0.0000	0.0000
	σ^2_e	0.0317	0.0316	0.0315	0.0254	0.0253	0.0238
	σ^2_p	0.0388	0.0388	0.0404	0.0338	0.0338	0.0344
	h^2_d	0.18±0.17	0.19±0.18	0.22±0.19	0.23±0.14	0.24±0.15	0.31±0.18
	h^2_m	-	-	-	0.06±0.11	0.07±0.11	0.06±0.11
	r_{dm}	-	-	-	-0.36±0.58	-0.43±0.51	-0.46±0.47
	c^2	-	-	-	0.00±0.06	0.00±0.06	0.00±0.06
	e^2	-	-	-	0.75±0.11	0.75±0.12	0.69±0.13
	$h^2_m+c^2$	-	-	-	0.06	0.07	0.06
	h^2_T	-	-	-	0.20	0.19	0.24
	-2 log l	-	-	-	-1809	-1793	-1851
CWW	σ^2_d	461	453	605	411	397	617
	σ^2_m	-	-	-	176	168	209
	σ_{dm}	-	-	-	-147	-140	-227
	σ^2_{pe}	-	-	-	0.08	0.03	0.03
	σ^2_e	1408	1406	1404	1088	1097	976
	σ^2_p	1869	1859	2009	1529	1522	1576
	h^2_d	0.25±0.19	0.24±0.19	0.30±0.20	0.27±0.16	0.26±0.16	0.39±0.21
	h^2_m	-	-	-	0.12±0.13	0.11±0.13	0.13±0.14
	r_{dm}	-	-	-	-0.55±0.38	-0.54±0.38	-0.63±0.28
	c^2	-	-	-	0.00±0.07	0.00±0.07	0.00±0.07
	e^2	-	-	-	0.71±0.12	0.72±0.12	0.62±0.15
	$h^2_m+c^2$	-	-	-	0.12	0.11	0.13
	h^2_T	-	-	-	0.18	0.18	0.24
	-2 log l	-	-	-	7019	6980	7086

PDG = Preweaning daily gain (5); CWW = 205-day weight (6)

σ^2_d = additive direct genetic variance (7); σ^2_m = maternal genetic variance (8); σ_{dm} direct maternal genetic covariance (9); σ^2_{pe} = maternal permanent environmental effect (10); σ^2_e = residual variance (11); σ^2_p = phenotypic variance (12); h^2_d = direct heritability (13); h^2_m = maternal heritability (14); r_{dm} = direct-maternal genetic correlation (15); c^2 = the ratio of the permanent environmental variance to the phenotypic variance (16); e^2 = the ratio of the residual variance to the phenotypic variance (17); h^2_T = total heritability (18)

7. táblázat A becsült genetikai paraméterek, variancia és kovariancia komponensek II.
tulajdonság (1); genetikai paraméter (2); apamodell (3); egyedmodell (4); választás előtti napi súlygyarapodás (5); 205-napos súly (6); direkt additív genetikai variancia (7); anyai genetikai variancia (8); direkt-anyai kovariancia (9); anyai állandó környezeti variancia (10); hiba variancia (11); fenotípusos variancia (12); direkt örökölhetőség (13); anyai örökölhetőség (14); direkt-anyai genetikai korreláció (15); állandó környezeti variancia aránya a fenotípusban (16); hiba variancia aránya a fenotípusban (17); teljes örökölhetőség (18)

Table 8

Breeding value of sires with model 2

ID of sire[&] (1)	B[*]	N[#]	Breeding value of sires with model 2 (2)							
			BW (kg)		WW (kg)		PDG (kg/day)		CWW (kg)	
			SM	AM	SM	AM	SM	AM	SM	AM
8812	LR	1	-1.16	0.05	30.00	3.11	0.187	0.005	38.87	2.24
9330	HS	3	5.21	1.38	-5.26	-3.75	0.039	-0.003	16.24	1.28
10166	LR	2	-6.92	-0.61	-6.73	-4.04	-0.006	-0.015	-8.25	-3.86
11010	HS	7	6.24	3.01	13.17	9.10	0.079	0.033	28.82	13.92
13184	HE	118	1.08	-1.11	-8.18	-24.45	-0.029	-0.082	0.62	-20.37
13201	HS	8	1.73	0.21	-36.8	-5.24	-0.109	-0.017	-39.73	-5.41
14111	HE	76	1.79	-0.88	11.50	6.52	0.072	0.065	22.40	12.08
14180	HS	2	-1.06	-1.54	34.39	5.94	0.120	0.006	6.93	-1.55
14213	AA	2	-4.22	-0.05	27.01	9.57	0.087	0.028	14.51	5.84
14282	HE	47	2.28	1.11	9.73	5.99	0.012	0.002	11.04	3.99
14347	BD	2	5.30	0.53	15.96	1.31	0.061	0.005	28.72	3.93
14427	HS	14	0.29	0.10	3.79	7.10	0.027	0.023	1.43	5.20
14684	LI	2	-3.95	-0.71	-9.47	-3.62	-0.035	-0.020	-23.43	-6.95
14765	LI	2	4.48	1.10	52.51	13.26	0.243	0.048	67.97	14.76
14957	CH	4	-3.80	-1.55	-1.58	3.02	0.003	0.017	-5.00	1.34
14992	CH	31	0.82	2.17	-24.4	-4.66	-0.125	-0.027	-25.06	-4.36
15087	AA	4	-3.16	-0.01	8.68	10.28	0.036	0.057	-6.69	7.41
16137	CH	4	-2.01	-0.15	-0.22	2.59	-0.004	0.005	-1.93	1.15
16477	BD	43	2.50	-0.53	1.72	-13.16	0.012	-0.048	6.00	-11.47
16528	HS	54	-2.38	-3.16	-32.7	-34.35	-0.147	-0.140	-36.74	-35.18
16558	CH	4	3.34	1.89	13.67	8.08	0.025	0.024	4.38	3.58
16772	RA	124	-0.65	1.30	-9.00	-0.62	-0.043	-0.001	-8.08	6.82
17110	HE	6	2.43	1.66	-9.41	1.12	-0.097	-0.007	-7.63	0.89
17179	RA	8	-3.27	-0.79	-22.3	0.72	-0.081	0.039	-30.45	1.50
17428	HE	35	1.93	1.53	-13.9	-9.28	-0.104	-0.054	-17.40	-12.88
17600	HS	52	-1.72	-2.11	3.48	11.08	0.029	0.072	4.38	11.73
18275	AA	29	-0.27	2.70	-22.3	-13.30	-0.155	-0.081	-32.12	-15.00
18320	RA	76	-1.94	0.80	-19.7	-2.52	-0.110	-0.004	-25.72	-0.82
18337	LI	47	-0.89	0.32	-12.3	-2.20	-0.036	-0.012	-5.75	0.58
19842	HG	45	0.42	0.15	-27.6	-5.05	-0.087	-0.020	-24.48	-4.46
20217	BD	16	-1.14	-1.58	15.57	5.44	0.086	0.029	21.39	7.52
21027	CH	13	-3.03	-2.12	-8.02	-1.63	-0.039	-0.009	-3.29	-0.19
21503	HE	5	1.59	0.75	28.78	17.88	0.091	0.067	28.07	15.97

[&]ID = identity number (3); [*]B = breed (4); [#]N = number of progeny (5); BW = birth weight (6); WW = weaning weight (7); PDG = preweaning daily gain (8); 205-day weight (9); SM = sire model (10); AM = animal model (11); HS = Hungarian Simmental (12); HG = Hungarian Grey (13); HE = Hereford; AA = Aberdeen Angus; RA = Red Angus; LR = Lincoln Red; SH = Shaver; LI = Limousin; CH = Charolais; BD = Blonde d'Aquitaine

8. táblázat Az apák 2-es modellel becsült tenyészértékei

apa KLSZ (1); 2-es modellel becsült tenyészérték (2); azonosító szám (központi lajstromszám) (3); fajta (4); ivadékok száma (5); születési súly (6); választási súly (7); választás előtti napi súlygyarapodás (8); 205-napos súly (9); apamodell (10); egyedmodell (11); magyar tarka (12); magyar szürke (13)

Table 9

The rank of sires with model 2

ID of sire[&] (1)	B[*]	N[#]	Rank of sires (2)							
			BW		WW		PDG		CWW	
			SM	AM	SM	AM	SM	AM	SM	AM
8812	LR	1	22	18	3	13	2	16	2	14
9330	HS	3	3	7	18	24	10	19	8	17
10166	LR	2	33	23	19	25	19	24	24	24
11010	HS	7	1	1	9	6	7	7	3	3
13184	HE	118	13	27	21	32	20	32	16	32
13201	HS	8	11	15	33	28	29	25	33	27
14111	HE	76	10	26	10	9	8	3	6	4
14180	HS	2	20	28	2	11	3	13	11	23
14213	AA	2	32	20	5	5	5	9	9	9
14282	HE	47	8	9	11	10	15	17	10	11
14347	BD	2	2	13	6	16	9	15	4	12
14427	HS	14	16	17	13	8	13	11	15	10
14684	LI	2	31	24	24	23	21	27	26	28
14765	LI	2	4	10	1	2	1	5	1	2
14957	CH	4	30	29	17	14	17	12	19	16
14992	CH	31	14	3	30	26	31	28	28	25
15087	AA	4	28	19	12	4	11	4	21	7
16137	CH	4	25	21	16	15	18	14	17	18
16477	BD	43	6	22	15	30	16	29	12	29
16528	HS	54	26	33	32	33	32	33	32	33
16558	CH	4	5	4	8	7	14	10	13	13
16772	RA	124	18	8	22	19	24	18	23	8
17110	HE	6	7	5	23	17	27	21	22	19
17179	RA	8	29	25	28	18	25	6	30	15
17428	HE	35	9	6	26	29	28	30	25	30
17600	HS	52	23	31	14	3	12	1	14	5
18275	AA	29	17	2	29	31	33	31	31	31
18320	RA	76	24	11	27	22	30	20	29	22
18337	LI	47	19	14	25	21	22	23	20	20
19842	HG	45	15	16	31	27	26	26	27	26
20217	BD	16	21	30	7	12	6	8	7	6
21027	CH	13	27	32	20	20	23	22	18	21
21503	HE	5	12	12	4	1	4	2	5	1

[&]ID = identity number (3); [*]B = breed (4); [#]N = number of progeny (5); BW = birth weight (6); WW = weaning weight (7); PDG = preweaning daily gain (8); 205-day weight (9); SM = sire model (10); AM = animal model (11); HS = Hungarian Simmental (12); HG = Hungarian Grey (13); HE = Hereford; AA = Aberdeen Angus; RA = Red Angus; LR = Lincoln Red; SH = Shaver; LI = Limousin; CH = Charolais; BD = Blonde d'Aquitaine

9. táblázat Az apák 2-es modellel becsült rangsora

apa KLSZ (1); 2-es modellel becsült rangsor (2); azonosító szám (központi lajstromszám) (3); fajta (4); ivadékok száma (5); születési súly (6); választási súly (7); választás előtti napi súlygyarapodás (8); 205-napos súly (9); apamodell (10); egyedmodell (11); magyar tarka (12); magyar szürke (13)

Table 10

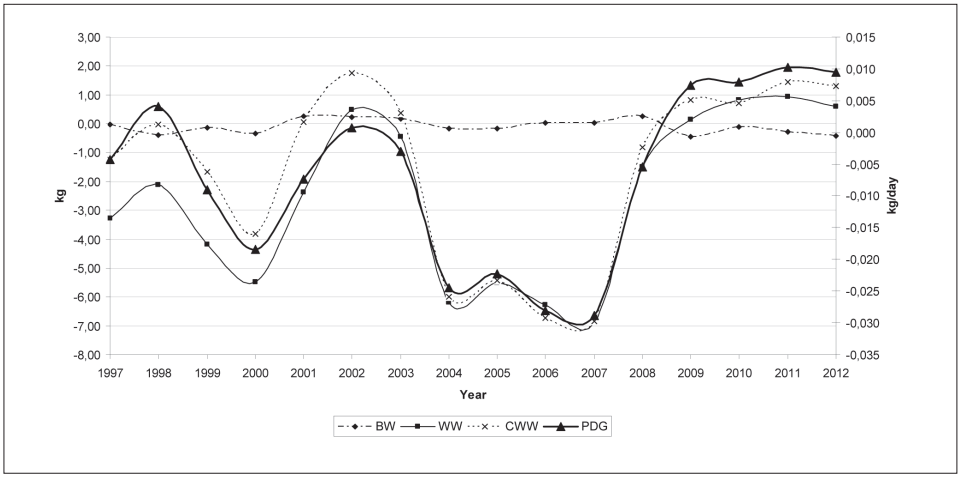
Rank correlation coefficients among the rank line of sires

Rank correlation		Animal model			
		BW	WW	PDG	CWW
Sire model	BW	*0.62			
	WW		*0.80		
	PDG			*0.72	
	CWW				*0.68

*p<0.01; BW = birth weight (1); WW = weaning weight (2); PDG = prewean. daily gain (3); 205-day weight (4)

10. táblázat Az apák rangsorai között számított rangkorrelációs együtthatók
szül. súly (1); választási súly (2); választás előtti napi súlygyarapodás (3); 205-napos súly (4)

Figure 1 **The genetic trend of the examined traits between 1997-2012**



BW=birth weight (1); WW=weaning weight (2); PDG=preweaning daily gain (3); CWW=205-day weight (4)

1. ábra: A vizsgált tulajdonságok genetikai trendje 1997-2012 között
születési súly (1); választási súly (2); vál. előtti napi súlygyarapodás (3); 205-napos súly (4)

Figure 1 shows the genetic trend. Birth weight show equable trend, the genetic value of this trait didn't change during the studied period. In contradiction weaning weight, preweaning daily gain and 205-day weaning weight shows decreasing trend as far as 2007 year, and increasing trend further on. The reasons for this situation is that France sires mostly Charolais were used in the herd to obtain crossbred progeny from 2007.

CONCLUSIONS

Direct heritability (h^2_d) value of weaning traits in the mixed, multibreed population was similar to the results in literature obtained by several authors. The maternal heritability (h^2_m) values, similarly to the literature, were lower than direct heritability values, one third of them. Notwithstanding, the maternal effect for calf weaning weight is not negligible when estimating breeding value.

Since values of relative error of heritability obtained in the study was quite high, generally higher than it was supposed in the single breed population, we have to take care during multibreed breeding value estimation. Namely, the result suggests that for the appropriate accuracy of multibreed breeding value estimation we have to have much larger population than in case of single breed breeding value estimation.

The comparison results of the applied three animal model resulted that model 2 was the most appropriate for multibreed breeding value estimation. This model takes the genotype of cows and calves, age cows and calves, year, birth season effects into consideration. So, animal model 2 can be suggested for multibreed breeding value estimation.

The relatively small differences in breeding values and sire ranks between sire and animal model call attention to the fact that using sire model in a certain circumstances may have an appropriate breeding value results.

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REFERENCES

Ahunu, B. K. - Arthur, P. F. - Kissiedu, H. W. A. (1997): Genetic and phenotypic parameters for birth and weaning weights of purebred and crossbred N'Dama and West African Shorthorn cattle. Liv. Prod. Sci., 51. 165-171.

Arnold, J. W. - Bertrand, J. K. - Benyshek, L. L. (1992): Animal model for genetic evaluation of multibreed data. J. Anim. Sci., 70. 3322-3332.

Bene Sz. - Komlósi I. - Nagy B. - Lengyel Z. - Szabó F. (2007): Többfajtás húsmarha tenyészértékbecslés a választási eredmények alapján. Állattenyésztés és Takarmányozás, 56. 521-539.

Bene, Sz. - Füller, I. - Fördős, A. - Szabó, F. (2010): Weaning results of beef Hungarian Fleckvieh calves. 2. Genetic parameters, breeding values. Arch. Tierz., 53. 26-36.

Bennett, G. L. - Gregory, K. E. (2001): Genetic (co)variances for calving difficulty score in composite and parental populations of beef cattle: II. Reproductive, skeletal, and carcass traits. J. Anim. Sci., 79. 52-59.

Boldman, K. G. - Kriese, L. A. - Van Vleck, L. D. - Kachman, S. D. (1993): A manual for use of MTDFREML. A set of programs to obtain estimates of variances and covariances. USDA-ARS, Clay Center, NE.

Cameron, N. D. (1997): Selection indices and prediction of genetic merit in animal breeding. CAB International.

Crews, D. H. - Kemp, R. A. (1999): Contributions of preweaning growth information and maternal effects for prediction of carcass trait breeding values among crossbred beef cattle. Can. J. Anim. Sci., 79. 17-25.

Cubas, A. C. - Berger, P. J. - Healey, M. H. (1991): Genetic parameters for calving ease and survival at birthh in Angus field data. J. Anim. Sci., 69. 3952-3958.

Dodenhoff, J. - Van Vleck, L. D. - Gregory, K. E. (1999): Estimation of direct, maternal and grandmaternal genetic effects for weaning weight in several breeds of beef cattle. J. Anim. Sci., 77. 840-845.

Duangjinda, M. - Bertrand, J. K. - Misztal, I. - Druet, T. (2001): Estimation of additive and nonadditive genetic variances in Hereford, Gelbvieh and Charolais by method „R". J. Anim. Sci., 79. 2997-3001.

Elzo, M. A. - Famula, T. R. (1985): Multibreed sire evaluation procedures within a country. J. Anim. Sci., 60. 942-952.

Falconer, D. S. - Trudy, F. C. M. (1996): Introduction to quantitative genetics. Longman Group Ltd., 4th Edition.

Gregory, K. E. - Cundiff, L. V. - Koch, R. M. (1995): Genetic and phenotypic (co)variances for growth and carcass traits of purebred and composite populations of beef cattle. J. Anim. Sci., 73. 1920-1926.

Gutiérrez, J. P. - Goyache, F. - Fernández, I. - Alvarez, I. - Royo, L. J. (2007): Genetic relationships among calving ease, calving interval, birth weight, and weaning weight in the Asturiana de los Valles beef cattle breed. J. Anim. Sci., 85. 69-75.

Harvey, W. R. (1990): User's guide for LSLMW and MIXMDL PC-2 version Mixed Model Least-Squares and Maximum Likelihood Computer Program. The Ohio State University. Colombus, OH

Lengyel Z. (2005): Húshasznú borjak választási eredményét befolyásoló környezeti és genetikai tényezők. Doktori (PhD) értekezés, Keszthely.

Meyer, K. - Carrick, M. J. - Donelly, B. J. P. (1993): Genetic parameters for growth traits of Australian beef cattle from a multibreed selection experiment. J. Anim. Sci., 71. 2614-2622.

Meyer, K. (1998): DFREML. Version 3.0. User Notes

Nagy, I. - Csató, L. - Farkas, J. - Gyovai, P. - Radnóczi, L. - Komlósi, I. (2008): Genetic parameters of direct and ratio traits from field and station tests of pigs. Arch. Tierz., 51. 172-178.

Newman, S. - Reverter, A. - Johnston, D. J. (2002): Purebred-crossbred performance and genetic evaluation of postweaning growth and carcass traits in Bos indicus × Bos taurus crosses in Australia. J. Anim. Sci., 80. 1801-1808.

Notter, D. R. - Cundiff, L. V. (1991): Across-breed expected progeny differences: use of within-breed expected progeny differences to adjust breed evaluations for sire sampling and genetic trend. J. Anim. Sci., 69. 4763-4776.

Núnez-Dominguez, R. - Van Vleck, L. D. - Boldman, K. G. - Cundiff, L. V. (1993): Correlations for genetic expression for growth of calves of Hereford and Angus dams using a multivariate animal model. J. Anim. Sci., 71. 2330-2340.

Núnez-Dominguez, R. - Van Vleck, L. D. - Cundiff, L. V. (1995): Prediction of genetic values of sires for growth traits of crossbred cattle using a multivariate animal model with heterogeneous variances. J. Anim. Sci., 73. 2940-2950.

Pollak, E. J. - Quaas, R. L. (1998): Multibreed genetic evaluation of beef cattle. In: Proc. 6th World Cong. Genet. Appl. Livest. Prod., Armidale, NSW, Australia. 23. 81-88.

Rodríguez-Almeida, F. A. - Van Vleck, L. D. - Gregory, K. E. (1997): Estimation of direct and maternal effects for prediction of expected progeny differences for birth and weaning weights in three multibreed populations. J. Anim. Sci., 75. 1203-1212.

Radnóczi L. - Kövér Gy. - Farkas J. - Nagy I. (2009): A hazai sertésállományok genetikai potenciáljának értékelése, teljesítményvizsgálati eredményeik alapján. Állattenyésztés és Takarmányozás. 58. 397-410.

Roso, V. M. - Schenkel, F. S. - Miller, S P. - Wilton, J. W. (2005): Additive, dominance, and epistatic loss effects on preweaning weight gain of crossbred beef cattle from different Bos taurus breeds. J. Anim. Sci., 83. 1780-1787.

Splan, R. K. - Cundiff, L. V. - Van Vleck, L. D. (1998): Genetic parameters for sex-specific traits in beef cattle. J. Anim. Sci., 76. 2272-2278.

Splan, R. K. - Cundiff, L. V. - Dikeman, M. E. - Van Vleck, L. D. (2002): Estimates of parameters between direct and maternal genetic effects for weaning weight and direct genetic effects for carcass traits in crossbred cattle. J. Anim. Sci., 80. 3107-3111.

Sullivan, P. G. - Wilton, J. W. - Miller, S. P. - Banks, L. R. (1999): Genetic trends and breed overlap derived from multiple - breed genetic evaluations of beef cattle for growth traits. J. Anim. Sci., 77. 2019-2027.

Szabó F. (1993): Fajtakülönbségek populációgenetikai elemzése a húsmarha tenyésztésben. Doktori értekezés, MTA

Szőke Sz. - Komlósi I. (2000): A BLUP modellek összehasonlítása. Állattenyésztés és Takarmányozás, 49. 231-246.

Tőzsér, J. - Balika, S. - Komlósi, I. (2003): Estimate of heritability of weaning weight in Limousine breed in Hungary. Bulletin of the Szent István University, 47-51.

Van Vleck, L. D. - Hakim, A. F. - Cundiff, L. V. - Koch, R. M. - Crouse, J. D. - Boldman, K. G. (1992): Estimated breeding values for meat characteristics of crossbred cattle with animal model. J. Anim. Sci., 70. 363-371.

Van Vleck, L. D. - Gregory, K. E. - Bennett, G. L. (1996): Direct and maternal covariances by age of dam for weaning weight. J. Anim. Sci., 74. 1801-1805.

Willham, R. L. (1972): The role of maternal effects in animal breeding: III. Biometrical aspects of maternal effects in animals. J. Anim. Sci., 35. 1288-1293.

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